

## SEQUENCE LISTING

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AOKI, TOSHIO  
AKASHI, TOMOYOSHI

<120> POLYNUCLEOTIDE ENCODING 2-HYDROXYISOFLAVANONE SYNTHASE

<130> JKM-001

<140> 09/890,646

<141> 2001-08-02

<150> PCT/JP00/00596

<151> 2000-02-04

<160> 14

<170> PatentIn Ver. 2.1

<210> 1

<211> 1895

<212> DNA

<213> Glycyrrhiza echinata

<220>

<221> CDS

<222> (144)..(1712)

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acttcctcct atactcgact ctttgttatt agttatcatt attattatta caccattaaa 120

gtagcaaaga tcaaacaaac acc atg ttg gtg gaa ctt gca att act ctg ttg 173

Met Leu Val Glu Leu Ala Ile Thr Leu Leu  
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gtg ata gcc ctg ttc ata cac ctg cgt ccc aca cta agt gca aaa tca 221

Val Ile Ala Leu Phe Ile His Leu Arg Pro Thr Leu Ser Ala Lys Ser  
15 20 25

aag tcc ctt cgc cac ctc cca aac cct cca agt cca aaa ccc cgt ctc 269

Lys Ser Leu Arg His Leu Pro Asn Pro Pro Ser Pro Lys Pro Arg Leu  
30 35 40

cca ttt gtg ggt cac ctt cac ctt tta gac aaa ccc ctt ctc cac tac 317

Pro Phe Val Gly His Leu His Leu Leu Asp Lys Pro Leu Leu His Tyr  
45 50 55

tcc ctc atc gac cta agc aaa cgc tat ggt ccg ctt tac tcc ctc tac 365

Ser Leu Ile Asp Leu Ser Lys Arg Tyr Gly Pro Leu Tyr Ser Leu Tyr  
60 65 70

ttc ggt tcc atg cca acc gtt gta gcc tcc acc cct gaa ctt ttc aaa 413

Phe Gly Ser Met Pro Thr Val Val Ala Ser Thr Pro Glu Leu Phe Lys  
75 80 85 90

ctc ttc ctc caa act cac gag gcc tct tcc ttc aac aca agg ttc caa	461
Leu Phe Leu Gln Thr His Glu Ala Ser Ser Phe Asn Thr Arg Phe Gln	
95 100 105	
acc tct gcc att agg cgc cta acc tac gac aac tct gtt gcc atg gtt	509
Thr Ser Ala Ile Arg Arg Leu Thr Tyr Asp Asn Ser Val Ala Met Val	
110 115 120	
ccc ttt ggt cct tac tgg aag ttc att agg aag ctc atc atg aac gac	557
Pro Phe Gly Pro Tyr Trp Lys Phe Ile Arg Lys Leu Ile Met Asn Asp	
125 130 135	
ctc ctc aat gcc aca act gtg aac aag ttg agg cct tta agg agc caa	605
Leu Leu Asn Ala Thr Thr Val Asn Lys Leu Arg Pro Leu Arg Ser Gln	
140 145 150	
gaa atc cga aag gtc ctc agg gtg atg gca cag agt gct gag tct cag	653
Glu Ile Arg Lys Val Leu Arg Val Met Ala Gln Ser Ala Glu Ser Gln	
155 160 165 170	
gtc cca ctt aat gtc acc gag gag ctt ctc aag tgg acc aac agc acc	701
Val Pro Leu Asn Val Thr Glu Glu Leu Leu Lys Trp Thr Asn Ser Thr	
175 180 185	
atc tcg agg atg atg ctt ggg gaa gca gag gaa atc agg gac ata gca	749
Ile Ser Arg Met Met Leu Gly Glu Ala Glu Glu Ile Arg Asp Ile Ala	
190 195 200	
cgt gac gtg ctt aag atc ttt ggg gag tat agt ctc acc gac ttc atc	797
Arg Asp Val Leu Lys Ile Phe Gly Glu Tyr Ser Leu Thr Asp Phe Ile	
205 210 215	
tgg ccc ttg aag aaa ctc aag gtt ggg caa tac gag aag agg att gac	845
Trp Pro Leu Lys Lys Leu Lys Val Gly Gln Tyr Glu Lys Arg Ile Asp	
220 225 230	
gat ata ttc aac agg ttt gac ccc gtc att gag agg gtc atc aag aaa	893
Asp Ile Phe Asn Arg Phe Asp Pro Val Ile Glu Arg Val Ile Lys Lys	
235 240 245 250	
aga cag gag att agg aag aag agg aag gag agg aat ggt gag atc gag	941
Arg Gln Glu Ile Arg Lys Lys Arg Lys Glu Arg Asn Gly Glu Ile Glu	
255 260 265	
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Glu Gly Glu Gln Ser Val Val Phe Leu Asp Thr Leu Leu Asp Phe Ala	
270 275 280	
gag gac gag acc atg gag atc aaa atc acc aag gaa caa atc aag ggc	1037
Glu Asp Glu Thr Met Glu Ile Lys Ile Thr Lys Glu Gln Ile Lys Gly	
285 290 295	
ctt gtt gtg gat ttc ttc tca gca ggg acg gat tcc acg gcg gtg gca	1085
Leu Val Val Asp Phe Phe Ser Ala Gly Thr Asp Ser Thr Ala Val Ala	
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aca gac tgg gct ctg tca gag ctc atc aac aac ccc agg gtg ttt caa	1133
Thr Asp Trp Ala Leu Ser Glu Leu Ile Asn Asn Pro Arg Val Phe Gln	
315 320 325 330	
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Lys Ala Arg Glu Glu Ile Asp Ala Val Val Gly Lys Asp Arg Leu Val	
335 340 345	
gac gag gca gat gtc cag aac ctt cct tac att aga tcc atc gtg aag	1229
Asp Glu Ala Asp Val Gln Asn Leu Pro Tyr Ile Arg Ser Ile Val Lys	
350 355 360	
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Glu Thr Phe Arg Met His Pro Pro Leu Pro Val Val Lys Arg Lys Cys	
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Val Gln Glu Cys Glu Val Asp Gly Tyr Val Ile Pro Glu Gly Ala Leu	
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Ile Leu Phe Asn Val Trp Ala Val Gly Arg Asp Pro Lys Tyr Trp Asp	
395 400 405 410	
agg ccc act gag ttc cgt ccc gaa agg ttc tta gaa aat gtg ggt gaa	1421
Arg Pro Thr Glu Phe Arg Pro Glu Arg Phe Leu Glu Asn Val Gly Glu	
415 420 425	
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Gly Asp Gln Ala Val Asp Leu Arg Gly Gln His Phe Gln Leu Leu Pro	
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Phe Gly Ser Gly Arg Arg Met Cys Pro Gly Val Asn Leu Ala Thr Ala	
445 450 455	
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Gly Met Ala Thr Leu Leu Ala Ser Val Ile Gln Cys Phe Asp Leu Ser	
460 465 470	
gta gtg ggc cca cag gga aag ata ttg aag ggc aat gat gcc aag gtt	1613
Val Val Gly Pro Gln Gly Lys Ile Leu Lys Gly Asn Asp Ala Lys Val	
475 480 485 490	
agc atg gaa gag aga gct gga ctc acg gtt cca agg gca cat aac ctc	1661
Ser Met Glu Glu Arg Ala Gly Leu Thr Val Pro Arg Ala His Asn Leu	
495 500 505	
atc tgt gtc ccg gtt gca aga tca agt gcc gta ccc aaa ctc ttt tcg	1709
Ile Cys Val Pro Val Ala Arg Ser Ser Ala Val Pro Lys Leu Phe Ser	
510 515 520	
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Ser	
ataataattt tcaataaggt atcaatcaat gatatataga caatgatacc catatatcat	1822
cttcgcgact agtctctctt tggtacagta tggttgtaaca gcttaaatct atataatttt	1882

tactcgcata tcc

1895

&lt;210&gt; 2

&lt;211&gt; 523

&lt;212&gt; PRT

&lt;213&gt; Glycyrrhiza echinata

&lt;400&gt; 2

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His	Leu	Arg	Pro	Thr	Leu	Ser	Ala	Lys	Ser	Lys	Ser	Leu	Arg	His	Leu
			20					25					30		

Pro	Asn	Pro	Pro	Ser	Pro	Lys	Pro	Arg	Leu	Pro	Phe	Val	Gly	His	Leu
		35					40					45			

His	Leu	Leu	Asp	Lys	Pro	Leu	Leu	His	Tyr	Ser	Leu	Ile	Asp	Leu	Ser
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Lys	Arg	Tyr	Gly	Pro	Leu	Tyr	Ser	Leu	Tyr	Phe	Gly	Ser	Met	Pro	Thr
65					70					75					80

Val	Val	Ala	Ser	Thr	Pro	Glu	Leu	Phe	Lys	Leu	Phe	Leu	Gln	Thr	His
				85					90					95	

Glu	Ala	Ser	Ser	Phe	Asn	Thr	Arg	Phe	Gln	Thr	Ser	Ala	Ile	Arg	Arg
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Leu	Thr	Tyr	Asp	Asn	Ser	Val	Ala	Met	Val	Pro	Phe	Gly	Pro	Tyr	Trp
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Lys	Phe	Ile	Arg	Lys	Leu	Ile	Met	Asn	Asp	Leu	Leu	Asn	Ala	Thr	Thr
	130					135						140			

Val	Asn	Lys	Leu	Arg	Pro	Leu	Arg	Ser	Gln	Glu	Ile	Arg	Lys	Val	Leu
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Arg	Val	Met	Ala	Gln	Ser	Ala	Glu	Ser	Gln	Val	Pro	Leu	Asn	Val	Thr
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Glu	Glu	Leu	Leu	Lys	Trp	Thr	Asn	Ser	Thr	Ile	Ser	Arg	Met	Met	Leu
		180					185						190		

Gly	Glu	Ala	Glu	Glu	Ile	Arg	Asp	Ile	Ala	Arg	Asp	Val	Leu	Lys	Ile
		195					200					205			

Phe	Gly	Glu	Tyr	Ser	Leu	Thr	Asp	Phe	Ile	Trp	Pro	Leu	Lys	Lys	Leu
	210					215						220			

Lys	Val	Gly	Gln	Tyr	Glu	Lys	Arg	Ile	Asp	Asp	Ile	Phe	Asn	Arg	Phe
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Asp	Pro	Val	Ile	Glu	Arg	Val	Ile	Lys	Lys	Arg	Gln	Glu	Ile	Arg	Lys
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 Ile Lys Ile Thr Lys Glu Gln Ile Lys Gly Leu Val Val Asp Phe Phe  
 290 295 300  
 Ser Ala Gly Thr Asp Ser Thr Ala Val Ala Thr Asp Trp Ala Leu Ser  
 305 310 315 320  
 Glu Leu Ile Asn Asn Pro Arg Val Phe Gln Lys Ala Arg Glu Glu Ile  
 325 330 335  
 Asp Ala Val Val Gly Lys Asp Arg Leu Val Asp Glu Ala Asp Val Gln  
 340 345 350  
 Asn Leu Pro Tyr Ile Arg Ser Ile Val Lys Glu Thr Phe Arg Met His  
 355 360 365  
 Pro Pro Leu Pro Val Val Lys Arg Lys Cys Val Gln Glu Cys Glu Val  
 370 375 380  
 Asp Gly Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn Val Trp  
 385 390 395 400  
 Ala Val Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Thr Glu Phe Arg  
 405 410 415  
 Pro Glu Arg Phe Leu Glu Asn Val Gly Glu Gly Asp Gln Ala Val Asp  
 420 425 430  
 Leu Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg  
 435 440 445  
 Met Cys Pro Gly Val Asn Leu Ala Thr Ala Gly Met Ala Thr Leu Leu  
 450 455 460  
 Ala Ser Val Ile Gln Cys Phe Asp Leu Ser Val Val Gly Pro Gln Gly  
 465 470 475 480  
 Lys Ile Leu Lys Gly Asn Asp Ala Lys Val Ser Met Glu Glu Arg Ala  
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<212> DNA

<213> Glycyrrhiza echinata

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caaggttagc atggaagaga gagctggact cacggttcca agggcacata acctcatctg 180
tgtcccgggt gcaagatcaa gtgccgtacc caaactcttt tcgtcgtaaa acatacgcgc 240
gacaccacag aaagttgcca tggcatgatg ctttttatat aataattttc aataagggtat 300
caatcaatga tatatagaca atgataccca tatatcatct tcacgactag tctctctttg 360
gtacagtatg ttgtaacagc ttaaattctat ataattttta ctcgcatatc catttcctga 420
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422

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<213> Artificial Sequence

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<220>
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<210> 5
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<220>
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<220>
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<220>
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<210> 9

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 9

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<210> 10

<211> 17

<212> DNA

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<223> Description of Artificial Sequence: Primer

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17

<210> 11

<211> 27

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<210> 13

<211> 27

<212> DNA

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<223> Description of Artificial Sequence: Primer

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27

<210> 14

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<212> DNA

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<223> Description of Artificial Sequence: Primer

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26